

AMENDMENTS TO THE SPECIFICATION

Please replace the paragraph starting on page 1, line 1, with the following:

This application is a continuation of U.S. Patent Application No. 09/804,690, filed March 12, 2001, which is a continuation of application Ser. No. 09/146,187, filed September 1, 1998, now U.S. Patent No. 6,248,523, which is a division of application Ser. No. 08/977,818, filed Nov. 25, 1997, now U.S. Pat. No. 5,807,995, which is a division of application Ser. No. 08/670,274, filed Jun. 13, 1996, now U.S. Pat. No. 5,891,668, which is a continuation-in-part of application Ser. No. 08/585,758, filed Jan. 16, 1996, U.S. Pat. No. 5,679,523 which claims the benefit of U.S. provisional patent application No. 60/006,856, filed Nov. 16, 1995, the disclosures of which are herein incorporated by reference.

Please replace the paragraph starting on page 6, line 3, with the following:

The full length human cDNA contains an ~~1140~~ 1170 bp open reading frame, encoding a ~~380~~ 390 amino acid protein (GenBank Accession No. U82130). The human and mouse cDNAs are 86% identical at the nucleotide level. The predicted proteins are 94% identical and are distinguished by 20 amino acid mismatches and one gap. A coiled-coil domain (human TSG101 aa 231-302) and a proline-rich domain (human TSG101 aa 130-205, 32% proline) typical of the activation domains of transcription factors are highly conserved between the human and mouse proteins, with only one amino acid mismatch in each of the two domains. The leucine zipper motif in the coiled-coil domain of the human TSG101 protein is identical to the one in the mouse protein.

Please replace the paragraph starting on page 33, line 22, with the following:

A 1494 bp cloned human cDNA insert (which was deposited under the Budapest Treaty at the American Type Culture Collection, Manassas, VA 20110-2209 on June 17, 2003 with Accession No. PTA-5265) was termed full length TSG101 cDNA. Sequence analysis of this cDNA identified a 1140 bp open reading frame predicted to encode a 380 amino acid protein with a molecular mass of 42.841 kDa and a pI of 5.87. The human and mouse cDNAs are 86% identical at the nucleotide level. The predicted proteins are 94% identical and are distinguished by 20 amino acid mismatches and one gap. A coiled-coil domain (human TSG101 aa 231-302) and a proline-rich domain (human TSG101 aa 130-205, 32% proline) typical of the activation domains of transcription factors are highly conserved

between the human and mouse proteins, with only one amino acid mismatch in each of the two domains. The leucine zipper motif in the coiled-coil domain of the human TSG101 protein is identical to the one in the mouse protein. Other conserved features identified in human TSG101 include seven putative protein kinase C phosphorylation sites (aa 11, 38, 86, 89, 215, 225, 357), five potential ~~ease~~ casein kinase II phosphorylation sites (aa 38, 210, 249, 265, 290) and three potential N-glycosylation sites (aa 44,150,297). Analysis of the human TSG101 cDNA and protein sequences by the BLAST program search of NCBI database did not reveal any significant homology with the sequences for any other human genes.

Please replace the nucleic acid sequence of SEQ ID NO:3 with the following:

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1  gaaggggtgtg cgattgtgtg ggacggtctg gggcagccca gcagcggctg accctctgcc
61  tgcgggggaag ggagtcgcca ggcggccgtc atggcgggtg cggagagcca gctcaagaaa
121 atgggtgtcca agtacaaata cagagaccta actgtacgtg aaactgtcaa tgttattact
181 ctatacaaag atctcaaacc tgttttggat tcatatgttt ttaacgatgg cagttccagg
241 gaactaatga acctcactgg aacaatccct gtgccttata gaggtaatac atacaatatt
301 ccaatatgcc tatggctact ggacacatac ccatataatc cccctatctg ttttgtaaag
361 cctactagtt caatgactat taaaacagga aagcatgttg atgcaaatgg gaagatatat
421 ctcccttatac tacatgaatg gaaacaccca cagtcagact tgttggggct tattcaggtc
481 atgattgtgg tatttggaaga tgaacctcca gtcttctctc gtcctatttc ggcacacctat
541 ccgccataacc aggcaacggg gccaccaaat acttctctaca tgccaggcat gccagggtgga
601 atctctccat acccatccgg ataccctccc aatcccagtg gttaccaggg ctgtccttac
661 ccacctgggtg gtccatatcc tgccacaaca agttctcagt acccttctca gcctcctgtg
721 accactgttg gtcccagtag ggatggcaca atcagcgagg acaccatccg agcctctctc
781 atctctgcgg tcagtgaaca actgagatgg cggatgaagg aggaaatgga tcgtgccag
841 gcagagctca atgccttgaa acgaacagaa gaagacctga aaaaggggtca ccagaaactg
901 gaagagatgg ttaccggttt agatcaagaa gtagccgagg ttgataaaaa catagaactt
961 ttgaaaaaga aggatgaaga actcagttct gctctggaaa aaatggaaaa tcagtctgaa
1021 aacaatgata tcgatgaagt tatcattccc acagctccct tatacaaaaa gatcctgaat
1081 ctgtatgcag aagaaaacgc tattgaagac actatctttt acttgggaga agccttgaga
1141 aggggcgtga tagacctgga tgcttctctg aagcatgtac gtcttctgtc ccgtaaacag
1201 ttccagctga gggcactaat gcaaaaagca agaaagactg ccggtctcag tgacctctac
1261 tgacttctct gataccagct ggaggttgag ctcttcttaa agtattcttc tcttctttt
1321 atcagtaggt gccagaata agttattgca gtttatcatt caagtgtaaa atattttgaa
1381 tcaataatat attttctgtt ttcttttggt aaagactggc ttttattaat gcactttcta
1441 tcctctgtaa actttttgtg ctgaatgttg ggactgctaa ataaaatttg tttt

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Please replace the amino acid sequence of SEQ ID NO:4 with the following:

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MAVSESQLKKMVSKEYKYRDLTVRETVNVITLYKDLKPVLD SYVFNDGSSREL MNLTGTIPV P YRGNTYN
IPICLWLLDTPYNPPICFVKPTSSMTIKTGKHVDANGKIYLPYLHEWKHPQSDLLGLIQVMIVVFGDEPPVFSR
PISASYPPYQATGPPNTSYMPGMPGGISPYPSGYPPNPSGYPGCPYPPGGPYPAT TSSQYPSQPPVTTVGPSRDG
TISED TIRASLISAVSDKLRWRMKEEMDRAQAE LNALKRTEEDLKKGHQKLEEMVTRLDQEVAEVDKNIELLKKK
DEELSSALEKMENQSENNDIDEV I IPTAPLYKQILNLYAEENAIEDTIFYLGEALRRGVIDLDVFLKHVRLLSRK
QFQLRALMQKARKTAGLS DLY

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